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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/735,357	12/12/2003	Yijia P. Bao	02-1227-A	2590

20306 7590 06/11/2007

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EXAMINER	
SISSON, BRADLEY L	
ART UNIT	PAPER NUMBER
1634	

MAIL DATE	DELIVERY MODE
06/11/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/735,357	BAO ET AL.	
	Examiner	Art Unit	
	/Bradley L. Sisson/	1634	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *24 May 2007*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-37,158 and 163-167* is/are pending in the application.

4a) Of the above claim(s) *9,11,14-17,19-22 and 163* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-8,10,12,13,18, 23-37,158 and 164-167* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *See Continuation Sheet*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

Continuation of Attachment(s) 3). Information Disclosure Statement(s) (PTO/SB/08), Paper No(s)/Mail Date :2/27/2004, 8/6/2004, 8/25/2004, 11/12/2004, 3/20/2006.

DETAILED ACTION

Election/Restrictions

1. Applicant's election of the species of:

a) One target nucleic acid;

b) Target nucleic acid is DNA;

c) Sample is contacted with substrate and then detector probe;

d) Photonic means of detection are used;

e) Detecting silver stain;

f) Biological complexity is 50,000 to $5x10^{10}$;

g) Target nucleic acid is part of a gene; and

h) Method used to distinguish between two or more species of a common genus, wherein the species differ by at least one nucleotide,

in the reply filed on 02 March 2007 is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)).

2. Claims 9, 11, 14-17, 19-22, and 163 are withdrawn from further consideration pursuant to 37 CFR 1.142(b) as being drawn to a nonelected invention, there being no allowable generic or linking claim. Election was made **without** traverse in the reply filed on 02 March 2007.

Specification

3. The use of the trademark TWEEN 20 has been noted in this application. It should be capitalized wherever it appears and be accompanied by the generic terminology.

4. Although the use of trademarks is permissible in patent applications, the proprietary nature of the marks should be respected and every effort made to prevent their use in any manner that might adversely affect their validity as trademarks.

Claim Rejections - 35 USC § 112

5. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

6. Claims 1-8, 10, 12, 13, 18, 23-37, 158, 164-167 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter, which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

7. As set forth in *Enzo Biochem Inc., v. Calgene, Inc.* (CAFC, 1999) 52 USPQ2d at 1135, bridging to 1136:

> To be enabling, the specification of a patent must teach those skilled in the art how to make and use the full scope of the claimed invention without 'undue experimentation.' " *Genentech, Inc. v. Novo Nordisk, A/S*, 108 F.3d 1361, 1365, 42 USPQ2d 1001, 1004 (Fed. Cir. 1997) (quoting *In re Wright*, 999 F.2d 1557, 1561, 27 USPQ2d 1510, 1513 (Fed. Cir. 1993)). Whether claims are sufficiently enabled by a disclosure in a specification is determined as of the date that the patent application was first filed, see *Hybritech, Inc. v. Monoclonal Antibodies, Inc.*, 802 F.2d 1367, 1384, 231 USPQ 81, 94 (Fed. Cir. 1986).... We have held that a patent specification complies with the statute

> even if a "reasonable" amount of routine experimentation is required in order to practice a claimed invention, but that such experimentation must not be "undue." See, *e.g.*, *Wands*, 858 F.2d at 736-37, 8 USPQ2d at 1404 ("Enablement is not precluded by the necessity for some experimentation . . . However, experimentation needed to practice the invention must not be undue experimentation. The key word is 'undue,' not 'experimentation.' ") (footnotes, citations, and internal quotation marks omitted). In *In re Wands*, we set forth a number of factors which a court may consider in determining whether a disclosure would require undue experimentation. These factors were set forth as follows: (1) the quantity of experimentation necessary, (2) the amount of direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the claims. *Id.* at 737, 8 USPQ2d at 1404. We have also noted that all of the factors need not be reviewed when determining whether a disclosure is enabling. See *Amgen, Inc. v. Chugai Pharm. Co., Ltd.*, 927 F.2d 1200, 1213, 18 USPQ2d 1016, 1027 (Fed. Cir. 1991) (noting that the *Wands* factors "are illustrative, not mandatory. What is relevant depends on the facts.").

The quantity of experimentation necessary

The quantity of experimentation necessary to enable the full scope of the claimed invention is great- on the order of several man-years, and then with little, if any, reasonable expectation of success.

The amount of direction or guidance presented / The presence or absence of working examples

The specification has been found to provide the following 7 examples:

Example 1, pp. 36-47, "Single-step and two-step hybridization methods for identifying SNPs in unamplified genomic DNA using Nanoparticle probes," (emphasis in the original);

Example 2, pp. 48-49, "Hybridization Conditions for method of the invention,"

Example 3, pp. 50-58, "Preparation f [*sic*; of] nanoparticle-oligonucleotide conjugated probes,"

Example 4, pp. 58-60, "Detection of mecA gene sequences from bacterial genomic DNA with gold nanoparticle probes,"

Example 5, pp. 60-62, "Staphylococcal speciation using bacterial genomic DNA an gold nanoparticle-labeled Tuf probes,"

Example 6, pp. 62-64, "Staphylococcal speciation and methicillin Resistance assay using PCR amplicons and gold nanoparticles labeled mecA and Tuf oligonucleotides as detection probes;" and

Example 7, pp. 64-65, "Staphylococcal speciation and methicillin resistance assay using genomic DNA and gold nanoparticle-labeled mecA, 16S and Tuf probes."

The nature of the invention

The invention relates to a method by which one is able to identify any single polynucleotide polymorphism in any organism, and/or differentiate between species of a genus where the "biological complexity ranges from 50,000 to 5,000,000,000," which fairly encompasses any and all viruses, bacterial, animals and plants.

The method also relates to performing amplification of the target nucleic acid, and that the amplification can be performed under virtually any condition, and any number of cycles.

The claimed invention also relates to sequencing a target nucleic acid.

The claimed invention also relates to the isolation and analysis of genomic DNA as found in a heterogeneous mixture.

The claimed invention also relates to the manufacture, use, and interpretation of data from arrays of capture probes, as well as the synthesis and use of detector probes, which again could be of virtually length.

The state of the prior art / The predictability or unpredictability of the art

Prior, as well as post-filing art teaches of numerous problems confronting those of ordinary skill in the art. These problems have not been addressed by the instant disclosure. Absent specific guidance as to how these issues are to be overcome, one of ordinary skill in the art would be forced to trial-and-error experimentation in an effort to overcome these known issues.

Zhang et al., *Bioinformatics*, Vol. 19, No. 1, 2003, page 14, states:

> It is widely recognized that the hybridization process is prone to errors and that the future of DNA sequencing by hybridization is predicated on the ability to successfully cope with such errors. However, the occurrence of hybridization errors results in the computational difficulty of the reconstruction of DNA sequencing by hybridization. The reconstruction problem of DNA sequencing by hybridization with errors is a strongly NP-hard problem. So far the problem has not been solved well.

Chan (US Patent Application Publication US 2002/0119455 A1):

> [0018] In practice, Probe Up methods have been used to generate sequences of about 100 base pairs. Imperfect hybridization has led to difficulties in generating adequate sequence. Error in hybridization is amplified many times. A 1% error rate reduces the maximum length that can be sequenced by at least 10%. Thus if 1% of 65,536 oligonucleotides gave false positive hybridization signals when hybridizing to a 200-mer DNA target, 75% of the scored "hybridizations" would be false (Bains, 1997). Sequence determination would be impossible in such an instance. The conclusion is that hybridization must be extremely effective in order to generate reasonable data. Furthermore, sequencing by hybridization also encounters problems when there are repeats in sequences that are one base less than the length of the probe. When such sequences are present, multiple possible sequences are compatible with the hybridization data. (Emphasis added.)

As set forth in Carrico, (US Patent 5,200,313) the extent and specificity of hybridization is affected by the following principal conditions:

- The purity of the nucleic acid preparation.

- Base compositions of the probe - G-C base pairs will exhibit greater thermal stability than A-T or A-U base pairs. Thus, hybridizations involving higher G-C content will be stable at higher temperatures.
- Length of homologous base sequences- any short sequence of bases (e.g., less than 6 bases), has a high degree of probability of being present in many nucleic acids. Thus, little or no specificity can be attained in hybridizations involving such short sequences. From a practical standpoint, a homologous probe sequence will often be between 300 and 1000 nucleotides.
- Ionic strength- the rate of reannealing increases as the ionic strength of the incubation solution increases. Thermal stability of hybrids also increases.
- Incubation temperature- Optimal reannealing occurs at a temperature about 25 - 30 °C below the melting temperature for a given duplex. Incubation at temperatures significantly below the optimum allows less related base sequences to hybridize.
- Nucleic acid concentration and incubation time- Normally, to drive the reaction towards hybridization, one of the hybridizable sample nucleic acid or probe nucleic acid will be present in excess, usually 100 fold excess or greater.
- Denaturing reagents- the presence of hydrogen bond-disrupting agents, such as formaldehyde and urea, increases the stringency of hybridization.
- Incubation- the longer the incubation time, the more complete will be the hybridization.
- Volume exclusion agents- the presence of these agents, as exemplified by dextran and dextran sulfate, are thought to increase the effective concentrations of the hybridizing elements thereby increasing the rate of resulting hybridizations.

- Further, subjecting the resultant hybridization product to repeated washes or rinses in heated solutions will remove non-hybridized probe. The use of solutions of decreasing ionic strength, and increasing temperature, e.g., 0.1X SSC for 30 minutes at 65 °C, will, with increasing effectiveness, remove non-fully complementary hybridization products.

Barany et al. (US 2007/0042419 A1), at paragraph 0036 teaches in part:

> For allele-specific oligonucleotide hybridization ("ASO"), the mutation must be known, hybridization and washing conditions must be known, cross-reactivity is difficult to prevent, closely-clustered sites due to interference of overlapping primers cannot undergo multiplex detection, and mutant DNA cannot be detected in less than 5% of background of normal DNA.

Choi et al. (US 2007/0042400 A1), at paragraph 0035, teach:

> [0035] In conventional methods of preparing nucleic acid, polysaccharides such as starch often co-precipitate with nucleic acid. When polysaccharides co-precipitate with nucleic acid, it is difficult to manipulate nucleic acids by amplification methods, such as PCR, or by other detection methods, such as hybridization detection. Polysaccharides may also inhibit digestion with restriction endonucleases and other enzymatic manipulations.

It is noted that the claimed method fairly encompasses the use of genomic DNA, and the use of an enzyme substrate as a label.

Yasuno et al., (US 2007/0031829 A1), paragraph 0037, teach in part:

> Certain oligonucleotides hybridize to polynucleotides having complementary sequences. Although DNA hybridization is sequence-specific, it is difficult to completely exclude hybridizations towards very similar nucleotide sequences.

Wang et al., (US 2007/0009954 A1), teach:

> [0004] A number of methods have been developed to score SNPs, including allele-specific hybridization, electrophoretic DNA sequencing, single-nucleotide extension using labeled chain terminators, the "Invader" assay (Third Wave Technologies, Madison Wis.), mass spectrometry, the 5' nuclease assay (Taqman; see below), etc. All of these

> methods entail assays that are either difficult or expensive to develop, or difficult or expensive to perform.

Rowlen et al., (US 2006/0286570 A1) teach:

> [0004] A variety of methods exist for detection of molecular recognition events. Detection of molecular recognition events such as DNA hybridization, antibody-antigen interactions, and protein-protein interactions becomes increasingly difficult as the number of recognition events to be detected decreases.

It is noted that the claimed method places no lower limit on the ability to accurately and reproducibly detect any binding between polymer and unit specific markers.

As evidenced above, the art is replete with known issues that directly impact the enablement of the claimed invention. A review of the instant disclosure fails to identify how these art-recognized issues are to be overcome such that the full scope of the invention can be practiced without the public having to resort to undue experimentation.

At column 40 of Jones (US Patent 5,858,671) the inherent obstacle in synthesizing oligonucleotide arrays is disclosed. As stated therein, "that even if the constituent enzymatic steps approach 100% completion, incompletely processed products can accumulate to significant levels. For example, during oligonucleotide synthesis of a 70-mer, requiring 69 couplings, a 99% coupling efficiency results in only 50% of the generated oligonucleotides being full length ($0.99^{69} = 0.50$)." In the present case, applicant is claiming a product that would be the result of an infinite number of couplings, not just 69 as described above.

8. The instant disclosure fails to teach how these art-recognized issues are to be overcome. Absent such guidance, one of skill in the art is forced to conduct trial-and-error experimentation. In view of the thousands of man-years that have already gone into this area of research, there is little likelihood that these issues will all be overcome through the expenditure of only routine optimization such that the full scope of the invention can be practiced. Assuming *arguendo* that these issues could be overcome, which is a position that the Office does not concede, the specification still does not provide the starting materials whereby any species of plant, virus, microbe, or animal can be "identified

9. The claimed method also encompasses the 'detection" of that which is not present (se preamble to claim 1). The specification is silent as to how one can detect that which is not present or would otherwise not provide any signal. Further, the specification has not set forth a reproducible procedure whereby one would be able to differentiate between background signal with no target present and where target is present, but at a very low copy number.

10. In view of the breadth of scope clamed, the limited guidance provided, the unpredictable nature of the art to which the claimed invention is directed, and in the absence of convincing evidence to the contrary, the claims are deemed to be non-enabled by the disclosure.

11. The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

12. Claims 1-9, 10, 12, 13, 23-37, 158, and 164-167 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

13. Claim 1 is confusing as to the use of the term "wild-type" to define "capture oligonucleotides." As seen in claim 1, part a), the "wild-type capture oligonucleotides" are to be complementary to a wild-type target nucleic acid and are to also be complementary to any number of mutant nucleotides found in the "wild-type." Seemingly the "wild-type" is not "wild-type" if it has mutant nucleotides. If in fact the "wild-type" does have "mutant" nucleotides, what then constitutes a "mutant" sequence?

14. Claim 1 is also confusing as to what constitutes the metes and bounds of "higher" as used in "higher biological complexity."

15. Claim 1 is confusing were in part c), line 4, is written "and to allow for." Perhaps applicant had intended to indicate >>and that which allows for<<.

16. Claim 1 is confusing as to how one is able to "detect" the "absence" of something.

17. Claims 2-9, 10, 12, 13, 23-37, 158, and 164-167, which depend from said claim 1, fail to overcome the above issues, and are similarly rejected.

18. Claims 24-26, 28, and 32-37 recite the limitation "the nanoparticles.". There is insufficient antecedent basis for this limitation in the claim. It is noted that claim 23 provides support for "nanoparticle probe."

Conclusion

19. Any inquiry concerning this communication or earlier communications from the examiner should be directed to /Bradley L. Sisson/ whose telephone number is (571) 272-0751. The examiner can normally be reached on 6:30 a.m. to 5 p.m., Monday through Thursday.

20. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ram Shukla can be reached on (571) 272-0735. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

21. Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

/Bradley L. Sisson/
Primary Examiner
Art Unit 1634

BLS